TEAM 4

PAGE: 1

RAW SEQUENCE LISTING
PATENT APPLICATION   *US/08/657,749*

DATE: 07/26/96
TIME: 11:14:39

*INPUT SET: S11781.raw*

> This Raw Listing contains the General
> Information Section and those Sequences
> containing ERRORS.

```
 1                                        SEQUENCE LISTING   Does Not Comply
 2                                                           Corrected Diskette Needed
 3    (1)    General Information:
 4
 5    (i) APPLICANTS:       Metz, James G.
 6                          Lardizabal, Kathryn D.
 7                          Lassner, Michael
 8
 9    (ii) TITLE OF INVENTION: Nucleic Acid Sequences Encoding
10                             a Plant Cytoplasmic Protein   Involved in
11                             Fatty Acyl-COA Metabolism
12
13    (iii) NUMBER OF SEQUENCES:  39
14
15    (iv) CORRESPONDENCE ADDRESS:
16
17        (A) ADDRESSEE:   Calgene, Inc.
18
19        (B) STREET:   1920 Fifth Street
20
21        (C) CITY:   Davis
22
23        (D) STATE:   CA
24
25        (E) COUNTRY:   USA
26
27        (F) ZIP:   95616
28
29    (v) COMPUTER READABLE FORM:
30
31        (A) MEDIUM TYPE:   Diskette, 3.50 inch, 1.0 MB
32
33        (B) COMPUTER:   Apple Macintosh
34
35        (C) OPERATING SYSTEM:   Macintosh 7.0
36
37        (D) SOFTWARE:   Microsoft Word 5.1a
38
39    (vi) PRIOR APPLICATION DATA:
40
41        (A) APPLICATION NUMBER:   PCT/US94/13686
42
43        (B) FILING DATE:   30-NOV-94
44
45        (C) CLASSIFICATION:
```

*See marked up notes throughout* →

```
46
47    (vii) CURRENT APPLICATION DATA:
48
49        (A) APPLICATION NUMBER:
50
51        (B) FILING DATE:
52
53        (C) CLASSIFICATION:
54
55    (vii) PRIOR APPLICATION DATA:
56
57        (A) APPLICATION NUMBER:  08/265,047
58
59        (B) FILING DATE:  23-JUN-94
60
61        (C) CLASSIFICATION:
62
63    (vii) PRIOR APPLICATION DATA:
64
65        (A) APPLICATION NUMBER:  08/160,602
66
67        (B) FILING DATE:  30-NOV-93
68
69        (C) CLASSIFICATION:
70
71    (vii) PRIOR APPLICATION DATA:
72
73        (A) APPLICATION NUMBER: 08/066,299
74
75        (B) FILING DATE:   20-MAY-93
76
77    (vii) PRIOR APPLICATION DATA:
78
79        (A) APPLICATION NUMBER: PCT/US92/09863
80
81        (B) FILING DATE:   13-NOV-92
82
83    (vii) PRIOR APPLICATION DATA:
84
85        (A) APPLICATION NUMBER:  07/933,411
86
87        (B) FILING DATE: 21-AUG-92
88
89    (vii) PRIOR APPLICATION DATA:
90
91        (A) APPLICATION NUMBER:  07/796,256
92
93        (B) FILING DATE:  20-NOV-91
94
95    (viii) ATTORNEY/AGENT INFORMATION:
96
97        (A) NAME:   Donna E. Scherer
98
```

*INPUT SET: S11781.raw*

```
 99        (B) REGISTRATION NUMBER:  34,719
100
101   (A) NAME:  Carl J. Schwedler
102
103   (B) REGISTRATION NUMBER:  36,924
104
105        (C) REFERENCE/DOCKET NUMBER:  CGNE 101-2 US
106
107   (ix) TELECOMMUNICATION INFORMATION:
108
109        (A) TELEPHONE:   (916) 753-6313
110
111        (B) TELEFAX:   (916) 753-1510
112
113
114
115   (2) INFORMATION FOR SEQ ID NO: : 1:
116
117   (i) SEQUENCE CHARACTERISTICS:
118
119        (A) LENGTH:   1786 base pairs
120
121        (B) TYPE:   nucleic acid
122
123        (C) STRANDEDNESS:  single
124
125        (D) TOPOLOGY:   linear
126
127   (ii) MOLECULE TYPE:   cDNA to mRNA
128
129   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
130
131   AAATCCTCCA CTCATACACT CCACTTCTCT CTCTCTCTCT CTCTCTCTGA AACAATTTGA    60
132
133
134   GTAGCAAACT TAAAAGAAA ATG GAG GAA ATG GGA AGC ATT TTA GAG TTT CTT   112
135                        Met Glu Glu Met Gly Ser Ile Leu Glu Phe Leu
136                         1               5                   10
137
138
139   GAT AAC AAA GCC ATT TTG GTC ACT GGT GCT ACT GGC TCC TTA GCA AAA   160
140   Asp Asn Lys Ala Ile Leu Val Thr Gly Ala Thr Gly Ser Leu Ala Lys
141            15              20                  25
142
143
144   ATT TTT GTG GAG AAG GTA CTG AGG AGT CAA CCG AAT GTG AAG AAA CTC   208
145   Ile Phe Val Glu Lys Val Leu Arg Ser Gln Pro Asn Val Lys Lys Leu
146            30              35                  40
147
148
149   TAT CTT CTT TTG AGA GCA ACC GAT GAC GAG ACA GCT GCT CTA CGC TTG   256
150   Tyr Leu Leu Leu Arg Ala Thr Asp Asp Glu Thr Ala Ala Leu Arg Leu
151            45              50                  55
```

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RAW SEQUENCE LISTING
PATENT APPLICATION   US/08/657,749

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*INPUT SET: S11781.raw*

```
152
153
154   CAA AAT GAG GTT TTT GGA AAA GAG TTG TTC AAA GTT CTG AAA CAA AAT          304
155   Gln Asn Glu Val Phe Gly Lys Glu Leu Phe Lys Val Leu Lys Gln Asn
156   60              65              70              75
157
158
159   TTA GGT GCA AAT TTC TAT TCC TTT GTA TCA GAA AAA GTG ACT GTA GTA          352
160   Leu Gly Ala Asn Phe Tyr Ser Phe Val Ser Glu Lys Val Thr Val Val
161                   80              85              90
162   CCC GGT GAT ATT ACT GGT GAA GAC TTG TGT CTC AAA GAC GTC AAT TTG          400
163   Pro Gly Asp Ile Thr Gly Glu Asp Leu Cys Leu Lys Asp Val Asn Leu
164           95              100             105
165
166
167   AAG GAA GAA ATG TGG AGG GAA ATC GAT GTT GTT GTC AAT CTA GCT GCT          448
168   Lys Glu Glu Met Trp Arg Glu Ile Asp Val Val Val Asn Leu Ala Ala
169           110             115             120
170
171
172   ACA ATC AAC TTC ATT GAA AGG TAC GAC GTG TCT CTG CTT ATC AAC ACA          496
173   Thr Ile Asn Phe Ile Glu Arg Tyr Asp Val Ser Leu Leu Ile Asn Thr
174           125             130             135
175
176
177   TAT GGA GCC AAG TAT GTT TTG GAC TTC GCG AAG AAG TGC AAC AAA TTA          544
178   Tyr Gly Ala Lys Tyr Val Leu Asp Phe Ala Lys Lys Cys Asn Lys Leu
179   140             145             150             155
180
181
182   AAG ATA TTT GTT CAT GTA TCT ACT GCT TAT GTA TCT GGA GAG AAA AAT          592
183   Lys Ile Phe Val His Val Ser Thr Ala Tyr Val Ser Gly Glu Lys Asn
184                   160             165             170
185
186
187   GGG TTA ATA CTG GAG AAG CCT TAT TAT ATG GGC GAG TCA CTT AAT GGA          640
188   Gly Leu Ile Leu Glu Lys Pro Tyr Tyr Met Gly Glu Ser Leu Asn Gly
189                   175             180             185
190
191
192   AGA TTA GGT CTG GAC ATT AAT GTA GAG AAG AAA CTT GTG GAG GCA AAA          688
193   Arg Leu Gly Leu Asp Ile Asn Val Glu Lys Lys Leu Val Glu Ala Lys
194                   190             195             200
195
196
197   ATC AAT GAA CTT CAA GCA GCG GGG GCA ACG GAA AAG TCC ATT AAA TCG          736
198   Ile Asn Glu Leu Gln Ala Ala Gly Ala Thr Glu Lys Ser Ile Lys Ser
199           205             210             215
200
201
202   ACA ATG AAG GAC ATG GGC ATC GAG AGG GCA AGA CAC TGG GGA TGG CCA          784
203   Thr Met Lys Asp Met Gly Ile Glu Arg Ala Arg His Trp Gly Trp Pro
204   220             225             230             235
```

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205
206
207   AAT GTG TAT GTA TTC ACC AAG GCA TTA GGG GAG ATG CTT TTG ATG CAA     832
208   Asn Val Tyr Val Phe Thr Lys Ala Leu Gly Glu Met Leu Leu Met Gln
209               240             245                 250
210
211
212   TAC AAA GGG GAC ATT CCG CTT ACT ATT ATT CGT CCC ACC ATC ATC ACC     880
213   Tyr Lys Gly Asp Ile Pro Leu Thr Ile Ile Arg Pro Thr Ile Ile Thr
214               255             260                 265
215
216
217   AGC ACT TTT AAA GAG CCC TTT CCT GGT TGG GTT GAA GGT GTC AGG ACC     928
218   Ser Thr Phe Lys Glu Pro Phe Pro Gly Trp Val Glu Gly Val Arg Thr
219               270             275                 280
220
221
222   ATC GAT AAT GTA CCT GTA TAT TAT GGT AAA GGG AGA TTG AGG TGT ATG     976
223   Ile Asp Asn Val Pro Val Tyr Tyr Gly Lys Gly Arg Leu Arg Cys Met
224       285             290                 295
225
226
227
228   CTT TGC GGA CCC AGC ACA ATA ATT GAC CTG ATA CCG GCA GAT ATG GTC    1024
229   Leu Cys Gly Pro Ser Thr Ile Ile Asp Leu Ile Pro Ala Asp Met Val
230   300             305                 310                 315
231
232
233   GTG AAT GCA ACG ATA GTA GCC ATG GTG GCG CAC GCA AAC CAA AGA TAC    1072
234   Val Asn Ala Thr Ile Val Ala Met Val Ala His Ala Asn Gln Arg Tyr
235               320             325                 330
236
237
238   GTA GAG CCG GTG ACA TAC CAT GTG GGA TCT TCA GCG GCG AAT CCA ATG    1120
239   Val Glu Pro Val Thr Tyr His Val Gly Ser Ser Ala Ala Asn Pro Met
240               335             340                 345
241
242
243   AAA CTG AGT GCA TTA CCA GAG ATG GCA CAC CGT TAC TTC ACC AAG AAT    1168
244   Lys Leu Ser Ala Leu Pro Glu Met Ala His Arg Tyr Phe Thr Lys Asn
245               350             355                 360
246
247
248   CCA TGG ATC AAC CCG GAT CGC AAC CCA GTA CAT GTG GGT CGG GCT ATG    1216
249   Pro Trp Ile Asn Pro Asp Arg Asn Pro Val His Val Gly Arg Ala Met
250               365             370                 375
251
252
253   GTC TTC TCC TCC TTC TCC ACC TTC CAC CTT TAT CTC ACC CTT AAT TTC    1264
254   Val Phe Ser Ser Phe Ser Thr Phe His Leu Tyr Leu Thr Leu Asn Phe
255   380             385                 390                 395
256
257
```

*INPUT SET: S11781.raw*

```
277
278  ATA GTT GAA GCT GAT ATG TTT TAC TTT GAT CCC AGG GCA ATT AAC TGG   1504
279  Ile Val Glu Ala Asp Met Phe Tyr Phe Asp Pro Arg Ala Ile Asn Trp
280  460             465             470             475
281
282
283
284  GAA GAT TAC TTC TTG AAA ACT CAT TTC CCA GGN GTC GTA GAG CAC GTT   1552
285  Glu Asp Tyr Phe Leu Lys Thr His Phe Pro Gly Val Val Glu His Val
286              480             485             490
287
288
289  CTT AAC TAAAAGTTAC GGTACGAAAA TGAGAAGATT GGAATGCATG CACCGAAAGN   1608
290  Leu Asn
291
292
293  NCAACATAAA AGACGTGGTT AAAGTCATGG TCAAAAAGA AATAAAATGC AGTTAGGTTT  1668
294
295
296  GTGTTGCAGT TTTGATTCCT TGTATTGTTA CTTGTACTTT TGATCTTTTT CTTTTTTAAT  1728
297
298
299  GAAATTTCTC TCTTTGTTTT GTGAAAAAAA AAAAAAAAAA GAGCTCCTGC AGAAGCTT    1786
300
301
```

---

```
986   (2) INFORMATION FOR SEQ ID NO: 15:
987
988   (i) SEQUENCE CHARACTERISTICS:
989
990      (A) LENGTH:17 base pairs
991
992      (B) TYPE: nucleic acid
993
994   (C) STRANDEDNESS:single
995
996      (D) TOPOLOGY:  linear
997
998   (ii) MOLECULE TYPE:  other
999
1000  (A) synthetic oligonucleotide
1001
1002  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15 :
1003
1004  AAYATHACNA CNYTNGG                                         17
1005
1006
1007
1008
```

*Description*

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```
1009  (2) INFORMATION FOR SEQ ID NO: 16:
1010
1011  (i) SEQUENCE CHARACTERISTICS:
```

*INPUT SET: S11781.raw*

```
1012
1013        (A) LENGTH:  17 base pairs
1014
1015        (B) TYPE:      nucleic acid
1016
1017   (C) STRANDEDNESS:single
1018
1019        (D) TOPOLOGY:   linear
1020
1021   (ii) MOLECULE TYPE: other
1022
1023   (A)synthetic oligonucleotide
1024
1025   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16 :
1026
1027
1028   SWRTTRCAYT TRAANCC                                         17
1029
1030
1031
```

*Description,* (handwritten annotation)

```
2114   (2) INFORMATION FOR SEQ ID NO: 25:
2115
2116   (i) SEQUENCE CHARACTERISTICS:
2117
2118        (A) LENGTH:  1664 base pairs
2119
2120        (B) TYPE:   nucleic acid
2121
2122         (C) STRANDEDNESS: single
2123
2124        (D) TOPOLOGY:  linear
2125
2126   (ii) MOLECULE TYPE:   cDNA to mRNA
2127
2128
2129
2130
2131    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:
2132
2133
2134   CA ATG ACG TCT GTG AAC GTA AAA CTC CTT TAC CAT TAC GTC ATA ACC   47
2135      Met Thr Ser Val Asn Val Lys Leu Leu Tyr His Tyr Val Ile Thr
2136      1           5               10              15
2137
2138
2139   AAC TTT TTC AAC CTC TGT TTC TTC CCA CTG ACG GGG ATC CTC GCC GGA   95
2140   Asn Phe Phe Asn Leu Cys Phe Phe Pro Leu Thr Gly Ile Leu Ala Gly
2141                    20              25              30
2142
2143
2144   AAA GGC TCT CGT CTT ACC ACA AAC GAT CTC CAC CAC TTC TAT TCA TAT   143
2145   Lys Gly Ser Arg Leu Thr Thr Asn Asp Leu His His Phe Tyr Ser Tyr
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*INPUT SET: S11781.raw*

```
2146                35                      40                      45
2147
2148
2149   CTC CAA CAC AAN CTT ATA ACC TTA ACC CTA CTC TTT GGC TTC ACC GTT   191
2150   Leu Gln His Xxx Leu Ile Thr Leu Thr Leu Leu Phe Gly Phe Thr Val
2151            50              55                      60
2152
2153
2154   TTT GGT TCG GTT CTC TAC TTC GTA ANC CGA CCC AAA CCG GTT TAC CTC   239
2155   Phe Gly Ser Val Leu Tyr Phe Val Xxx Arg Pro Lys Pro Val Tyr Leu
2156            65              70                      75
2157
2158
2159   GTT GAC TAC TCC TGC TAC CTT CCA CCA CAA CAT CTT AGC GCT GGT ATC   287
2160   Val Asp Tyr Ser Cys Tyr Leu Pro Pro Gln His Leu Ser Ala Gly Ile
2161   80                  85                  90                  95
2162
2163
2164   TCT AAG ACC ATG GAA ATC TTT TAT CAA ATA AGA AAA TCT GAT CCT TTA   335
2165   Ser Lys Thr Met Glu Ile Phe Tyr Gln Ile Arg Lys Ser Asp Pro Leu
2166                100                 105                 110
2167
2168
2169   CGA AAC GTG GCA TTA GAT GAT TCG TCT TCT CTT GAT TTC TTG AGA AAG   383
2170   Arg Asn Val Ala Leu Asp Asp Ser Ser Ser Leu Asp Phe Leu Arg Lys
2171                115                 120                 125
2172
2173
2174   ATT CAA GAG CGT TCA GGT CTA GGC GAT GAA ACC TAC GGC CCC GAG GGA   431
2175   Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr Tyr Gly Pro Glu Gly
2176                130                 135                 140
2177
2178
2179   CTG TTT GAG ATT CCT CCG AGG AAG AAT TTA GCG TCG GCG CGT GAA GAG   479
2180   Leu Phe Glu Ile Pro Pro Arg Lys Asn Leu Ala Ser Ala Arg Glu Glu
2181        145                 150                 155
2182
2183
2184
2185
2186   ACG GAG CAA GTA ATC AAC GGT GCG CTA AAA AAT CTA TTC GAG AAC AAC   527
2187   Thr Glu Gln Val Ile Asn Gly Ala Leu Lys Asn Leu Phe Glu Asn Asn
2188   160                 165                 170                 175
2189
2190
2191   AAA GTT AAC CCT AAA GAG ATT GGT ATA CTT GTG GTG AAC TCA AGC ATG   575
2192   Lys Val Asn Pro Lys Glu Ile Gly Ile Leu Val Val Asn Ser Ser Met
2193                180                 185                 190
2194
2195
2196   TTT AAT CCG ACT CCT TCG TTA TCC GCG ATG GTA GTT AAT ACT TCC AAG   623
2197   Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Ser Lys
2198                195                 200                 205
```

```
2199
2200
2201    CTC CGA AGC AAC ATC AAA AGC TTT AAT CTT GGA GGA ATG GGT TGC AGT    671
2202    Leu Arg Ser Asn Ile Lys Ser Phe Asn Leu Gly Gly Met Gly Cys Ser
2203            210             215             220
2204
2205
2206    GCT GGT GTT ATC GCC ATT GAT CTA GCT AAA GAC TTG TTG CAT GTT CAT    719
2207    Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His
2208            225             230             235
2209
2210
2211    AAA AAC ACA TAT GCT CTT GTG GTG AGC ACA GAG AAC ATC ACT CAA AAC    767
2212    Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Gln Asn
2213    240             245             250             255
2214
2215
2216    ATT TAT ACC GGT GAT AAC AGA TCC ATG ATG GTT TCG AAT TGC TTG TTC    815
2217    Ile Tyr Thr Gly Asp Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe
2218                    260             265             270
2219
2220
2221    CGT GTC GGT GGG GCA GCG ATT CTG CTC TCC AAC AAG CCG GGG GAT CGA    863
2222    Arg Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Pro Gly Asp Arg
2223                    275             280             285
2224
2225
2226    AGA CGG TCC AAG TAC AAG CTA GCT CAC ACG GTT CGA ACG CAT ACC GGA    911
2227    Arg Arg Ser Lys Tyr Lys Leu Ala His Thr Val Arg Thr His Thr Gly
2228            290             295             300
2229
2230
2231    GCT GAC GAC AAG TCT TTT GGA TGT GTG CGG CAA GAA GAA GAT GAT AGC    949
2232    Ala Asp Asp Lys Ser Phe Gly Cys Val Arg Gln Glu Glu Asp Asp Ser
2233            305             310             315
2234
2235
2236    GGT AAA ACC GGA GTT AGT TTG TCA AAA GAC ATA ACC GTT GTT GCC GGG    1007
2237    Gly Lys Thr Gly Val Ser Leu Ser Lys Asp Ile Thr Val Val Ala Gly
2238    320             325             330             335
2239
2240
2241    ATA ACG GTT CAG AAA AAC ATA ACA ACA TTG GGT CCG TTG GTT CTT CCT    1055
2242    Ile Thr Val Gln Lys Asn Ile Thr Thr Leu Gly Pro Leu Val Leu Pro
2243                    340             345             350
2244
2245
2246    CTG AGC GAA AAA ATC CTT TTT GTC GTT ACA TTC GTA GCC AAG AAA CTA    1103
2247    Leu Ser Glu Lys Ile Leu Phe Val Val Thr Phe Val Ala Lys Lys Leu
2248            355             360             365
2249
2250
2251
```

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RAW SEQUENCE LISTING
PATENT APPLICATION *US/08/657,749*

DATE: 07/26/96
TIME: 11:15:23

*INPUT SET: S11781.raw*

```
2252   TTA AAA GAT AAG ATC AAA CAC TAT TAC GTG CCG GAT TTC AAA CTT GCA   1151
2253   Leu Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala
2254           370             375             380
2255
2256
2257   GTA GAT CAT TTC TGT ATT CAT GCG GGA GGT AGA GCC GTG ATA GAT GTG   1199
2258   Val Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Val
2259           385             390             395
2260
2261
2262   TTA GAG AAG AAC TTA GGG CTA TCG CCG ATA GAT GTG GAG GCA TCA AGA   1247
2263   Leu Glu Lys Asn Leu Gly Leu Ser Pro Ile Asp Val Glu Ala Ser Arg
2264   400             405             410             415
2265
2266
2267   TCA ACA TTA CAT AGA TTT GGG AAT ACA TCG TCT AGT TCA ATT TGG TAT   1295
2268   Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr
2269               420             425             430
2270
2271
2272   GAA TTA GCA TAC ATA GAG CCA AAA GGA AGG ATG AAG AAA GGT AAT AAA   1343
2273   Glu Leu Ala Tyr Ile Glu Pro Lys Gly Arg Met Lys Lys Gly Asn Lys
2274           435             440             445
2275
2276
2277   GCT TGC CAA ATA GCT GGT GGG TCA GGT TTT AAG TGT AAT AGT GCG GTT   1391
2278   Ala Cys Gln Ile Ala Gly Gly Ser Gly Phe Lys Cys Asn Ser Ala Val
2279           450             455             460
2280
2281
2282   TGG GTC GCT TTA CGC AAT GTC GAG GCT TCA GCT AAT AGT CCT TGG GAA   1439
2283   Trp Val Ala Leu Arg Asn Val Glu Ala Ser Ala Asn Ser Pro Trp Glu
2284           465             470             475
2285
2286
2287   CAT TGC ATT CAC AAA TAT CCG GTT CAA ATG TAT TCT GGT TCA TCA AAG   1487
2288   His Cys Ile His Lys Tyr Pro Val Gln Met Tyr Ser Gly Ser Ser Lys
2289   480             485             490             495
2290
2291
2292   TCA GAG ACT CCT GTC CAA AAC GGT CGG TCC TAATTTATGT ATCTCAAATG   1537
2293   Ser Glu Thr Pro Val Gln Asn Gly Arg Ser
2294               500
2295
2296
2297
2298   ATGTTGTCCA CTTTCTCTTT TTTTTTTTCT TTTTTTAGTT ATAATTTAAT GGTTACGATG   1597
2299
2300
2301   TTTTGTCTAG GTCGTTATAA ATAAAGAATA CATGGGTGTT ACTAGTATAA AAAAAAAAAA   1657
2302
2303
2304   AAAAAAA                                                             1664
```

2305
2306

---

2627    (2) INFORMATION FOR SEQ ID NO: 30:
2628
2629     (i) SEQUENCE CHARACTERISTICS:
2630
2631        (A) LENGTH:   42 base pairs
2632
2633        (B) TYPE: nucleic acid
2634
2635    (C) STRANDEDNESS:single
2636
2637        (D) TOPOLOGY:  linear
2638
2639     (ii) MOLECULE TYPE:  other
2640
--> **2641    (A)synthetic oligonucleotide**
2642
2643
2644     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:
2645
2646    CAUCAUCAUC AUGTCGACAA AATGACGTCC ATTAACGTAA AG                    42
2647
2648
2649

*same error*

---

2650    (2) INFORMATION FOR SEQ ID NO: 31:
2651
2652     (i) SEQUENCE CHARACTERISTICS:
2653
2654        (A) LENGTH:    50 base pairs
2655
2656        (B) TYPE: nucleic acid
2657
2658    (C) STRANDEDNESS:single
2659
2660        (D) TOPOLOGY:  linear
2661
2662     (ii) MOLECULE TYPE:  other
2663
--> **2664    (A)synthetic oligonucleotide**
2665
2666
2667     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31 :
2668
2669    CUACUACUAC UAGTCGACGG ATCCTATTTG GAAGCTTTGA CATTGTTTAG            50
2670
2671
2672
2673

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2696    (2) INFORMATION FOR SEQ ID NO: 33:

```
2697
2698    (i) SEQUENCE CHARACTERISTICS:
2699
2700       (A) LENGTH:  41 base pairs
2701
2702       (B) TYPE: nucleic acid
2703
2704    (C) STRANDEDNESS:single
2705
2706       (D) TOPOLOGY:  linear
2707
2708    (ii) MOLECULE TYPE:  other
2709
2710    (A)synthetic oligonucleotide
2711
2712    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33 :
2713
2714    CAUCAUCAUC AUGAATTCAA GCTTAARYTN BKNTAYCAYT A               41
2715
2716
2717
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```
2738    (2) INFORMATION FOR SEQ ID NO: 35:
2739
2740     (i) SEQUENCE CHARACTERISTICS:
2741
2742        (A) LENGTH: 41 base pairs
2743
2744        (B) TYPE: nucleic acid
2745
2746    (C) STRANDEDNESS:single
2747
2748        (D) TOPOLOGY:  linear
2749
2750     (ii) MOLECULE TYPE:  other
2751
2752    (A)synthetic oligonucleotide
2753
2754     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35 :
2755
2756    CAUCAUCAUC AUGAATTCAA GCTTAAYYTN GGNGGNATGG G               41
2757
2758
2759
```

```
2760    (2) INFORMATION FOR SEQ ID NO: 36:
2761
2762     (i) SEQUENCE CHARACTERISTICS:
2763
2764        (A) LENGTH: 40 base pairs
2765
2766        (B) TYPE: nucleic acid
2767
```
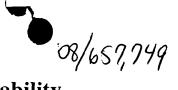
*INPUT SET: S11781.raw*

```
2768    (C) STRANDEDNESS:single
2769
2770       (D) TOPOLOGY:  linear
2771
2772    (ii) MOLECULE TYPE:  other
2773
2774    (A)synthetic oligonucleotide
2775
2776    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36 :
2777
2778    CUACUACUAC UAGGATCCGT CGACCCATNC CNCCNARRTT                40
2779
2780
```

```
2800    (2) INFORMATION FOR SEQ ID NO: 38:
2801
2802    (i) SEQUENCE CHARACTERISTICS:
2803
2804       (A) LENGTH:   41 base pairs
2805
2806       (B) TYPE: nucleic acid
2807
2808    (C) STRANDEDNESS:single
2809
2810       (D) TOPOLOGY:  linear
2811
2812    (ii) MOLECULE TYPE:  other
2813
2814    (A)synthetic oligonucleotide
2815
2816    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38 :
2817
2818    CUACUACUAC UAGGATCCGT CGACSWRTTR CAYTTRAANC C            41
2819
2820
2821
```

```
2822    (2) INFORMATION FOR SEQ ID NO: 39:
2823
2824    (i) SEQUENCE CHARACTERISTICS:
2825
2826       (A) LENGTH:   29 base pairs
2827
2828       (B) TYPE: nucleic acid
2829
2830    (C) STRANDEDNESS:single
2831
2832       (D) TOPOLOGY:  linear
2833
2834    (ii) MOLECULE TYPE:  other
2835
2836    (A)synthetic oligonucleotide
2837
```

# Notice of Availability

Applicant Aid for Biotechnology Computer Readable Form (CRF)
Sequence Listings Submissions

The Patent and Trademark Office (PTO) has developed a computer
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      Phone number:  703-305-8950
      Cost: Free-of-charge
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      Login as "anonymous".  Software is in directory /pub/checker
      Cost: Free-of-charge
3)    For diskette copies, telephone requests to 703-306-2600.
      Cost: $25.00

*For Further Information Contact:* Meredith Beckhardt at 703-308-4212.

```
2838    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39 :
2839
2840    CUACUACUAC UASWRTTRCA YTTRAANCC                                    29
2841
```